A Richards Growth Model to Predict Fruit Weight

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Precision Grape Yield Analyser

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Project initiated and coordinated by:

Further project partners:

Objective

- Predicting fruit weight at harvest time based on observations early in the growing season
- Using nonlinear growth models to describe the expected weights
- Bayesian modelling, using historical data and prior information (expert knowledge)

The Richards Growth Curve

The Richards model can be written as a differential equation

$$\frac{df}{dx} = \frac{\kappa}{1-\delta} f \left[\left(\frac{f}{\alpha} \right)^{\delta - 1} - 1 \right]$$

- α denotes the final size
- the point of inflection is determined by $f = \alpha \delta^{\frac{1}{1-\delta}}$
- κ acts as a scale parameter on x

The Richards Growth Curve

Jorgensen [1981, *The New Zealand Statistician* 16:5-15] found the solution

$$f(x) = \alpha \left[1 + (\delta - 1)e^{-\kappa(x-\gamma)}\right]^{\frac{1}{1-\delta}},$$

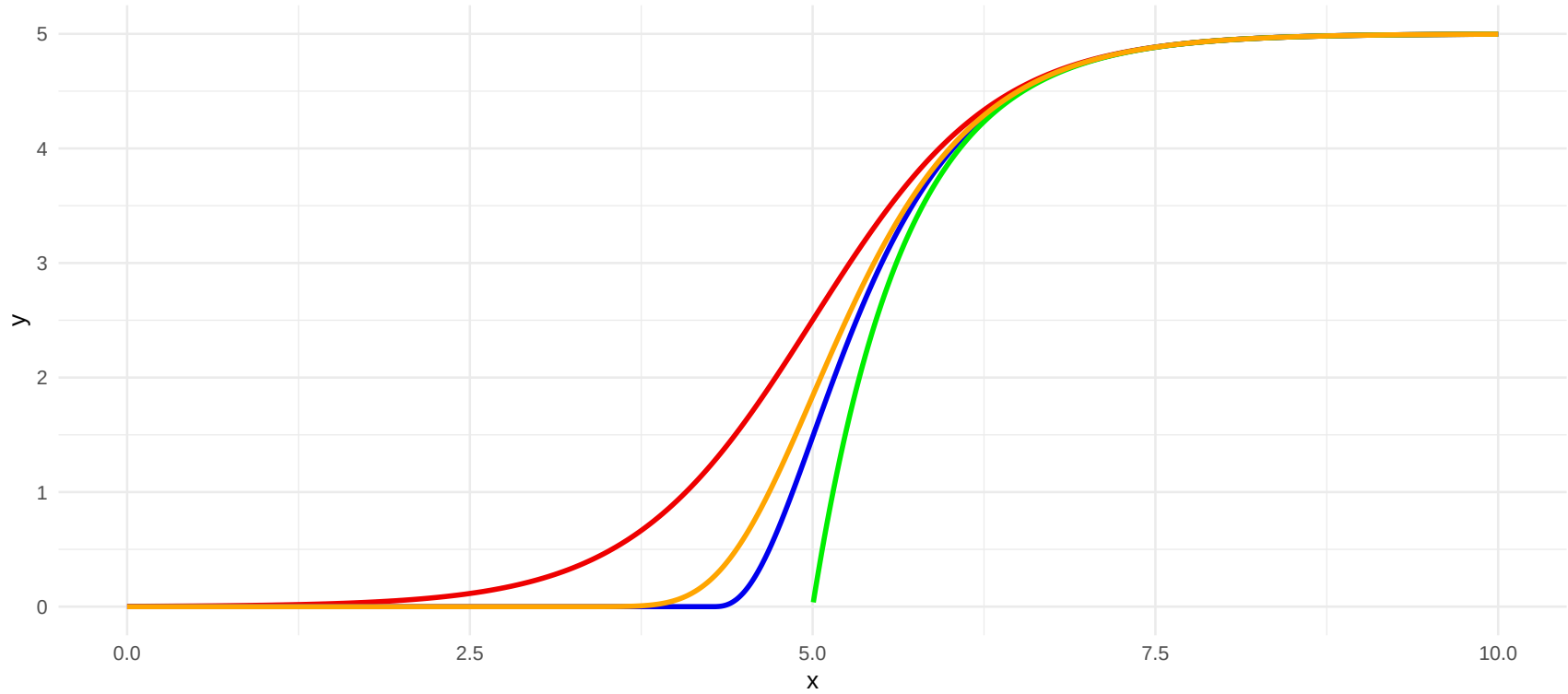
where

- $\delta \neq 1$
- for $\delta < 1$ the restriction $(1 - \delta)e^{\kappa\gamma} \leq 1$ is required to ensure that $0 \leq f \leq \alpha$
- $x = \gamma$ is the location of the inflection point

Growth Curves

It is easy to see that this parameterisation includes several popular growth curves, with the

- logistic model at $\delta = 2$,
- the Gompertz model at $\lim \delta \to 1$,
- the von Bertalanffy model at $\delta = \frac{2}{3}$,
- and the monomolecular model at $\delta = 0$.



Separating different curves

Discriminating between monomolecular-type models and curves, which asymptotically approach 0.

$$f_1(x|\cdot) = \alpha_1 \left[1 + (\delta_1 - 1)e^{-\kappa_1(x-\gamma_1)}\right]^{\frac{1}{1-\delta_1}} \quad \text{for } \delta_1 > 1$$

$$f_2(x|\cdot) = \begin{cases} \alpha_2 \left[1 + (\delta_2 - 1)e^{-\kappa_2(x-\gamma_2)}\right]^{\frac{1}{1-\delta_2}} & \text{for } -1 < \delta_2 < 1 \wedge x > \gamma_2 \\ 0 & \text{otherwise} \end{cases}$$

Advantages:

- $f(x)$ not defined at $\delta = 1$
- $f_2(x)$ more complicated to fit with additional constraints

Disadvantages:

- Two instead of one model

Bayesian Model

Given a sample (y_i, x_i) with $i \in \{1, 2, \ldots, N\}$, we assume the Bayesian model

$$y_i | x_i, \alpha, \delta, \kappa, \gamma \sim N\left(f(x_i|\cdot), \sigma^2\right)$$

with either the parameters of f_1 or f_2.

For the Richards curve parameters, the following prior distributions are specified:

$$\alpha \sim N\left(\mu_\alpha, \sigma_\alpha^2\right)_0^\infty \qquad \kappa \sim N\left(\mu_\kappa, \sigma_\kappa^2\right)_0^\infty \qquad \gamma \sim N\left(\mu_\gamma, \sigma_\gamma^2\right)_0^\infty$$

$$\delta_1 \sim N\left(\mu_{\delta_1}, \sigma_{\delta_1}^2\right)_1^\infty \qquad \delta_2 \sim N\left(\mu_{\delta_2}, \sigma_{\delta_2}^2\right)_{-1}^1$$

Model Selection

Predictive stacking with exact leave-one-out cross-validation, selecting the 'best' model as the model with the largest estimated weight.

Stacking of point estimates

The stacking weights for $k = 1, \ldots, K$ models are obtained by minimising the mean squared error

$$\hat{\omega} = \arg\min_{\omega} \sum_{i=1}^{N} \left(y_i - \sum_{k=1}^{k} \omega_k \hat{f}_k^{(-i)}(x_i) \right)^2$$

Stacking of predictive distributions (Yao et al. 2018)

Weights are the solution to the optimisation problem

$$\max_{\omega} \frac{1}{N} \sum_{i=1}^{N} \log \sum_{k=1}^{k} \omega_k p\left(y_i | y_{-i}, M_k\right)$$

Simulation Study

Estimating model weights for an arbitrary choice of parameter values, varying δ.

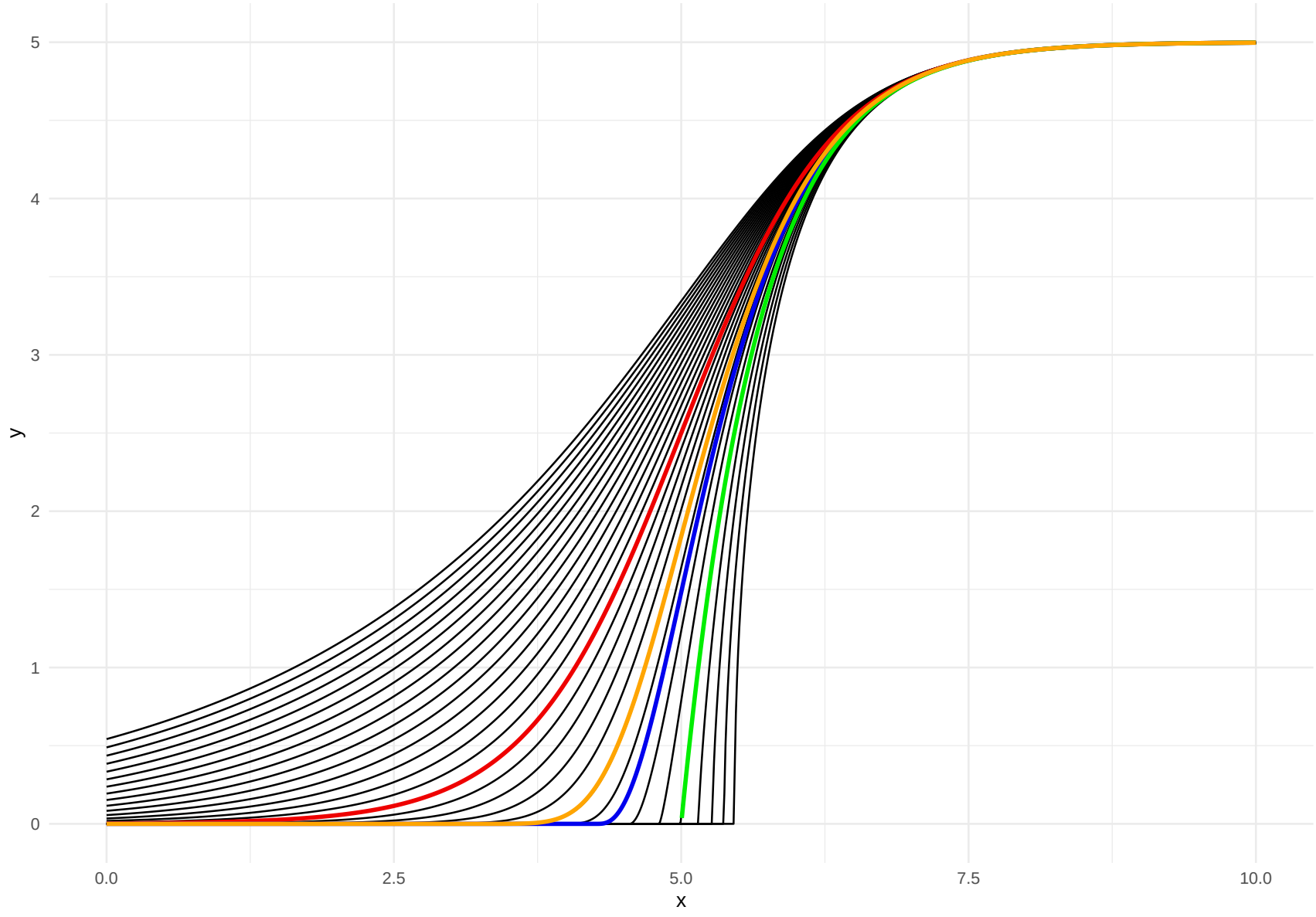
Set of three models:

- $f_1(x)$
- $f_2(x)$
- $f(x|\delta = 2)$ (logistic curve)

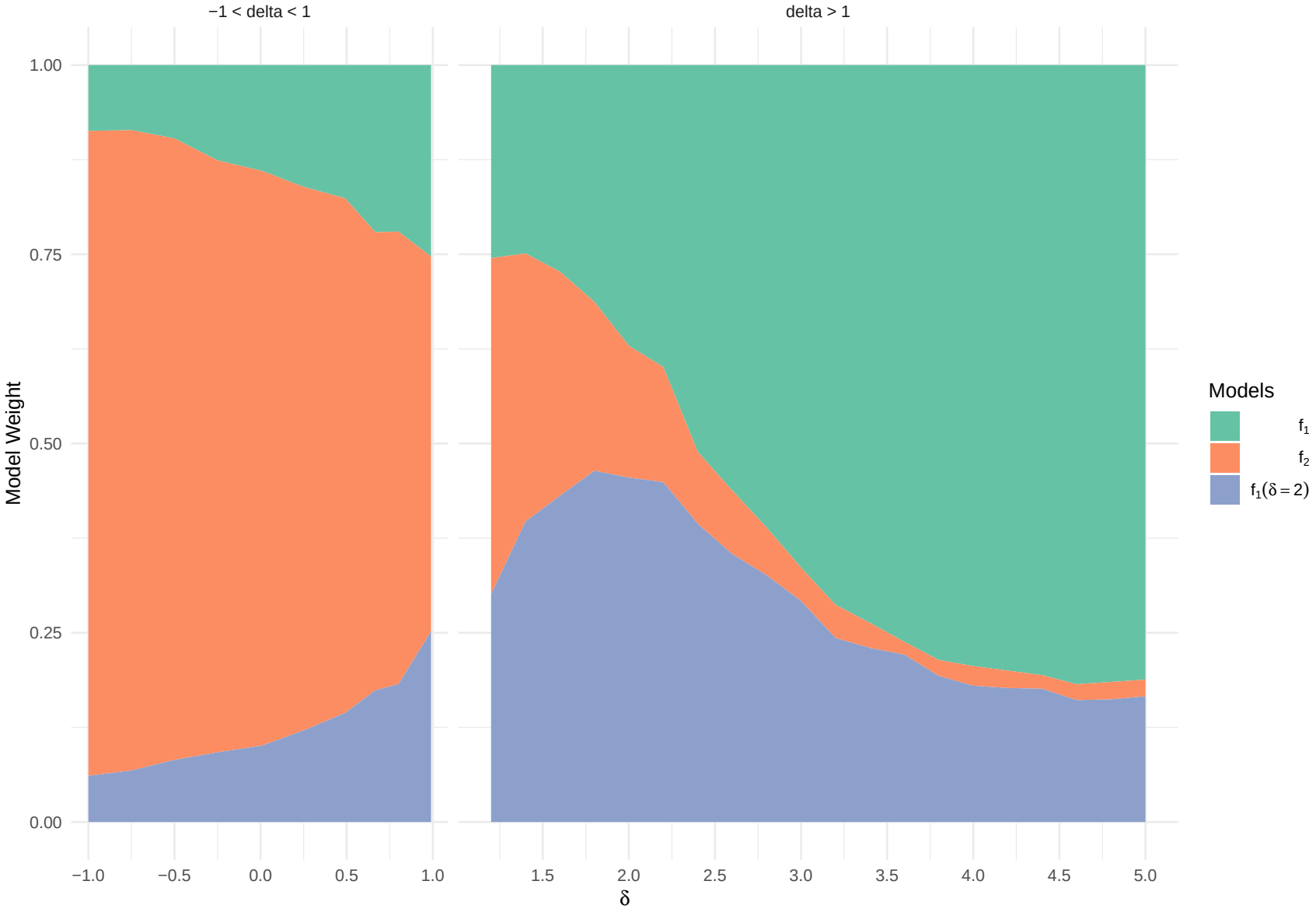
Settings:

- $N = 10$
- 1000 replications for each δ
- one chain with 10000 iterations
- (9000 burn-in, no thinning)

Simulation Settings



Simulation Results



A Double Richards Curve

We can assume that some fruit growth follows a double sigmoidal function, with a rest phase in-between, i.e. see Coombe and McCarthy (2000).

Two Richards curves can be combined by

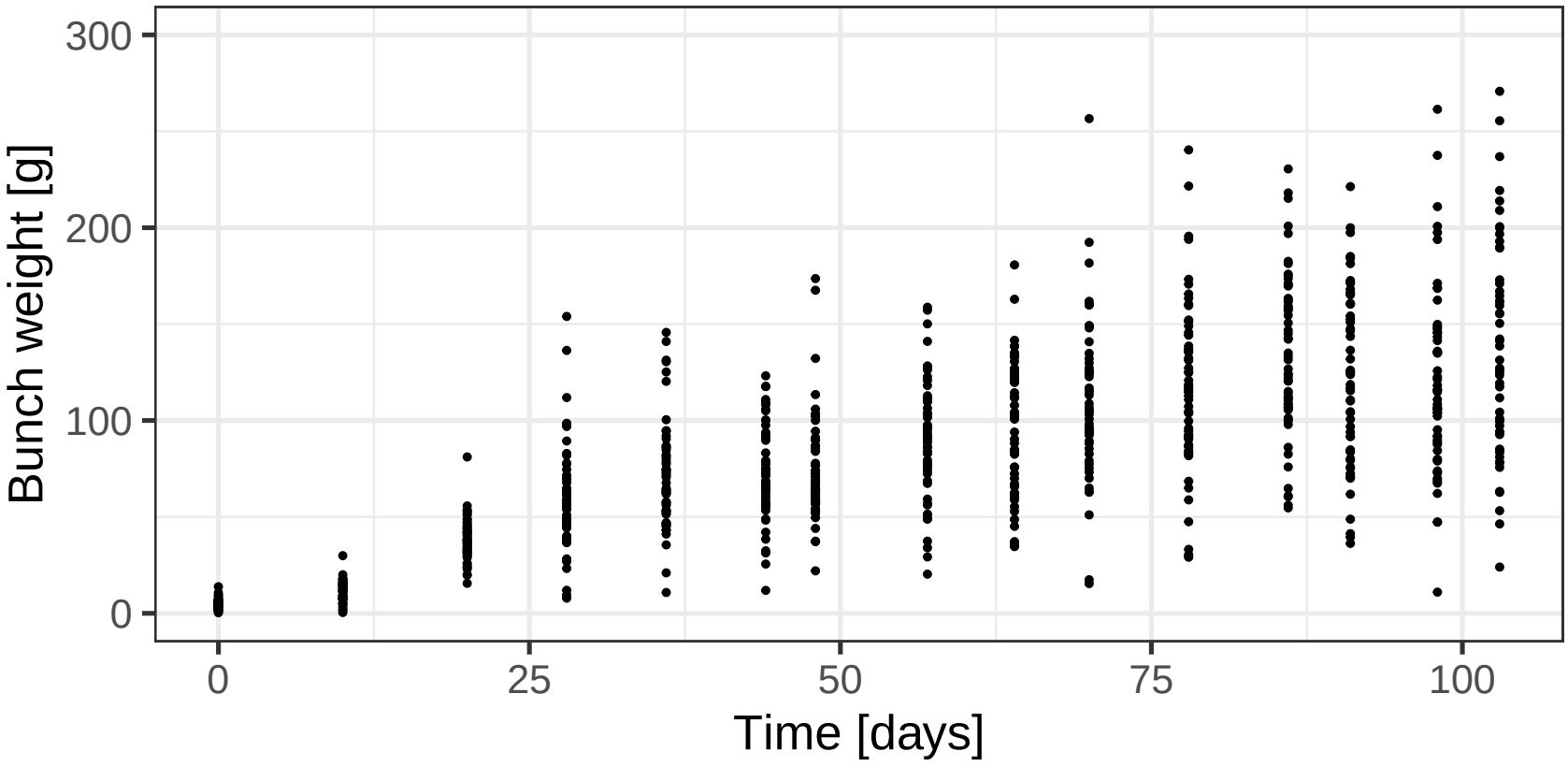
$$f(t;\cdot) = f^{(1)}(t;\cdot) + f^{(2)}(t;\cdot)$$

where $f^{(i)}(t;\cdot)$ is the Richards curve representing the first or second growth phase.

Data Example

Grape bunch weight was observed at the Rowley Crescent vineyard, Wairau Plains, Marlborough, New Zealand.

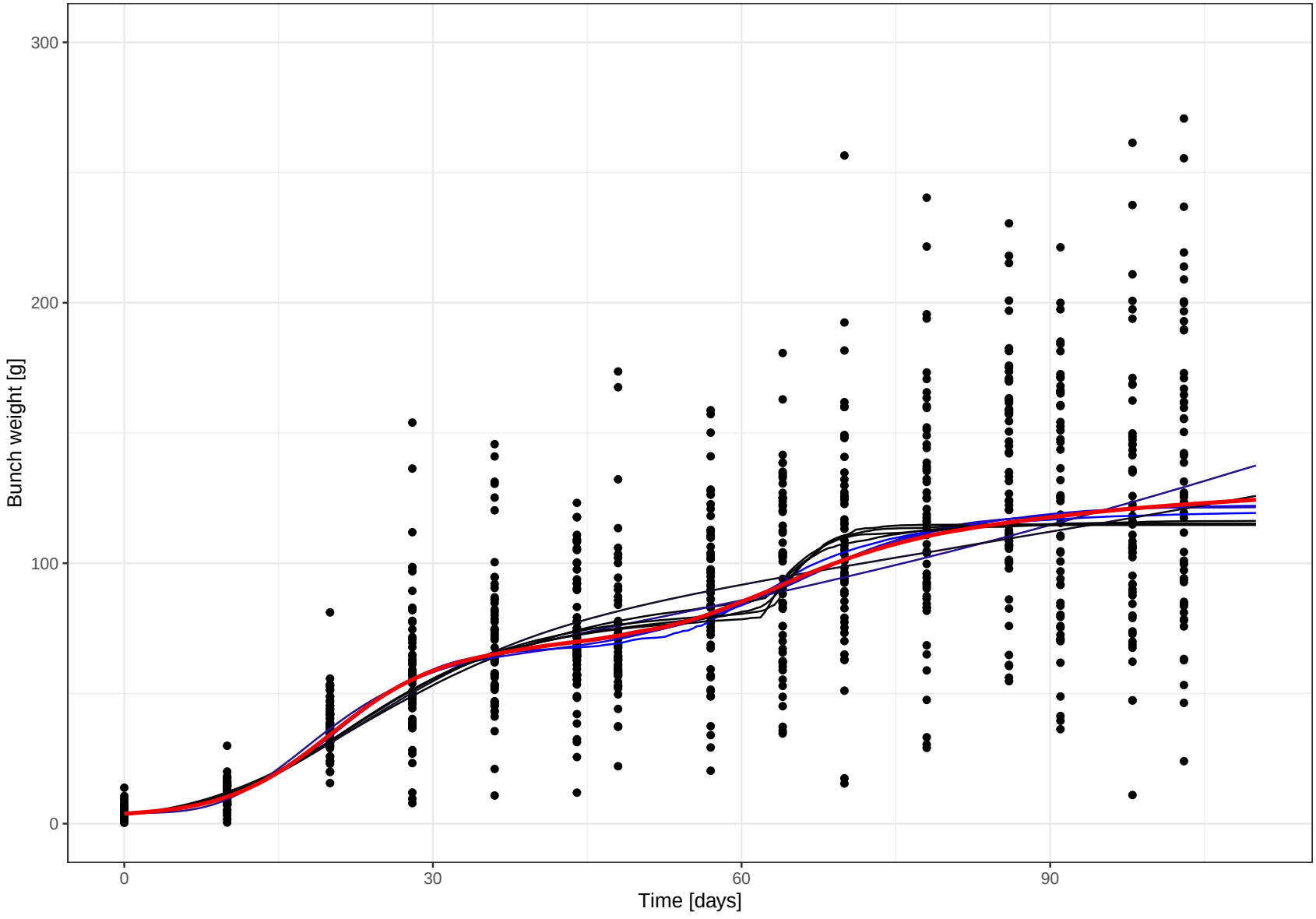
- weekly samples over the growing period 2017/18
- a subset of the data with apical bunches
- logarithmic transformation was applied to the observed weights



Stacking weights

Phase I	Phase II	Model weight
$\delta > 1$	$-1 < \delta < 1$	0.292
$\delta > 1$	$\delta = 2$	0.247
$\delta > 1$	$\delta > 1$	0.244
$-1 < \delta < 1$	$\delta > 1$	0.175
$-1 < \delta < 1$	$\delta = 2$	0.039
$\delta = 2$	$-1 < \delta < 1$	0.004
$-1 < \delta < 0$	$-1 < \delta < 1$	0.000
$\delta = 2$	$\delta > 1$	0.000
$\delta = 2$	$\delta = 2$	0.000

Model Predictions



References

- Coombe, B. G. and McCarthy, M. (2000).
  Dynamics of grape berry growth and physiology of ripening.
  Australian Journal of Grape and Wine Research, 6(2):131-135.
- Jorgensen, M. A. (1981).
  Fitting animal growth curves.
  The New Zealand Statistician, 16:5-15.
- Richards, F. J. (1959).
  A flexible growth curve for empirical use.
  Journal of Experimental Botany, 10(2):290-300.
- Vehtari, A., Gelman, A., and Gabry, J. (2017).
  Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC.
  Statistics and Computing, 27(5):1413-1432.
- Yao, Y., Vehtari, A., Simpson, D., and Gelman, A. (2018).
  Using stacking to average Bayesian predictive distributions.
  Bayesian Analysis, 13(3):917-1007.